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*Published in:*
Book of Abstracts. DTU's Sustain Conference 2015

*Publication date:*
2015

*Document Version*
Publisher's PDF, also known as Version of record

# Differential expression of small RNAs under chemical stress and fed-batch fermentation in *Escherichia coli*

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Abstract

Background: Bacterial small RNAs (sRNAs) are recognized as posttranscriptional regulators involved in the control of bacterial lifestyle and adaptation to stressful conditions. Although chemical stress due to the toxicity of precursor and product compounds is frequently encountered in microbial bioprocessing applications, the involvement of sRNAs in this process is not well understood. We have used RNA sequencing to map sRNA expression in *E. coli* under chemical stress and high cell density fermentation conditions with the aim of identifying sRNAs involved in the transcriptional response and those with potential roles in stress tolerance.

Results: RNA sequencing libraries were prepared from RNA isolated from *E. coli* K-12 MG1655 cells grown under high cell density fermentation conditions or subjected to chemical stress with twelve compounds including four organic solvent-like compounds, four organic acids, two amino acids, geraniol and decanoic acid. We have discovered 253 novel intergenic transcripts with this approach, adding to the roughly 200 intergenic sRNAs previously reported in *E. coli*. There are eighty-four differentially expressed sRNAs during fermentation, of which the majority are novel, supporting possible regulatory roles for these transcripts in adaptation during different fermentation stages. There are a total of 139 differentially expressed sRNAs under chemical stress conditions, where twenty-nine exhibit significant expression changes in multiple tested conditions, suggesting that they may be involved in a more general chemical stress response. Among those with known functions are sRNAs involved in regulation of outer membrane proteins, iron availability, maintaining envelope homeostasis, as well as sRNAs incorporated into complex networks controlling motility and biofilm formation.

Conclusions: This study has used deep sequencing to reveal a wealth of hitherto undescribed sRNAs in *E. coli* and provides an atlas of sRNA expression during seventeen different growth and stress conditions. Although the number of novel sRNAs with regulatory functions is unknown, several exhibit specific expression patterns during high cell density fermentation and are differentially expressed in the presence of multiple chemicals, suggesting they may play regulatory roles during these stress conditions. These novel sRNAs, together with specific known sRNAs, are candidates for improving stress tolerance and our understanding of the *E. coli* regulatory network during fed-batch fermentation.